

National Center for Genome Analysis Support (NCGAS) use and development of Tripal Genome Browsers on XSEDE's Jetstream

Sheri Sanders
Bioinformatics Analyst
NCGAS @ IU
ss93@iu.edu



What is NCGAS?

The mission of the National Center for Genome Analysis Support is to enable the biological research community of the US to **analyze, understand, and make use of the vast amount of genomic information now available.**

See ncgas.org for all our PAG talks!



Hosting Browsers

NCGAS has hosted JBrowse instances for years, but in the last ~year, we've moved to Tripal-based genome sites.

Currently, we develop/host resource sites for various projects in daphnia, coffee, peanut, junco, and pumillio frog among others.

Coffea Genomics Resource

Powered by NCGAS @ Indiana University

Home

Genome Browsers

Search Tools

Analyses

Downloads

Contacts

Genome Browsers

Analyses Described

BLAST Server



New Assembly for Coffee - September

A newly assembled version of the *C. arabica* genome has been completed, adding in PacBio data.

Publications


Downloads

Contacts

User menu

[My account](#)

[Log out](#)



Daphnia Genome Browser

NCGAS @ Indiana University

Home

Tools

Downloads

About

Home

Daphniagenomes.org is being currently developed to serve as a hub for Daphnia information. We currently serve jbrowse genome browsers for the TCO and PA42 assemblies, as well as the D. magna assembly, with plans to extend coverage to new daphnia species/assemblies as they are released. These browsers enable the viewing and sharing of genomic data for these assemblies as it is generated. Additionally, assembly specific tools such as BLAST searches are available and soon to be backed by the computation power of XSEDE's Jetstream Cloud (hosted at Indiana University).

Daphniagenomes.org is built using tripal and jbrowse, part of the Generic Model Organism Database (GMOD) community toolset.

JBrowse


BLAST

Recent Pubs

BioProjects

Downloads

NCGAS Home



Dark Eyed Junco Genome Resources

Powered by NCGAS @ Indiana University

HOME

GENOME BROWSER

BLAST

Welcome to the Dark Eyed Junco Genome Resource Page

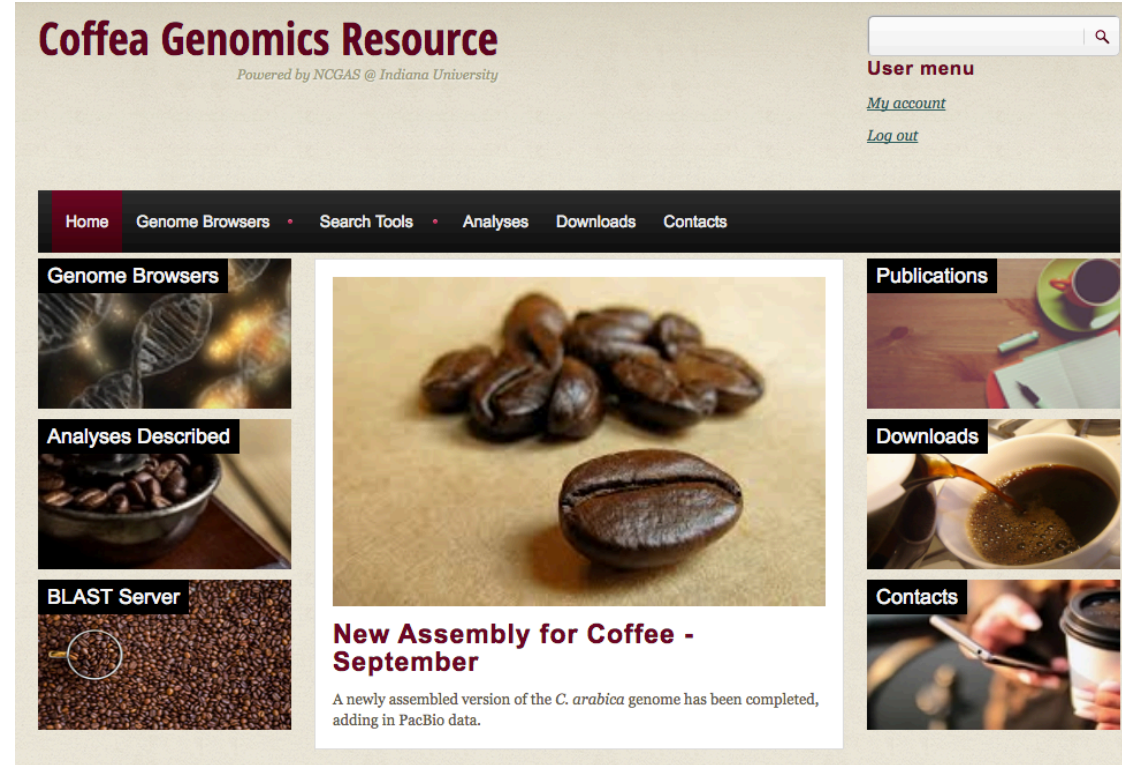
More will be added here soon!

Hosting Browsers

NCGAS has hosted JBrowse instances for years, but in the last ~year, we've moved to Tripal-based genome sites.

Currently, we develop/host resource sites for various projects in daphnia, coffee, peanut, junco, and pumillio frog among others.

Many of groups lack command line skills, so a main goal is to make things automated, more GUI oriented, or just generally easier to implement (in the beginning).



Welcome to the Dark Eyed Junco Genome Resource Page
More will be added here soon!

Tools: Tripal_blast tweak

We modified the tripal_blast module to build links to **show blast results in internal/external JBrowse sites** through URL manipulation.

As a quirk of how it is written, it doesn't require you to own the target JBrowse instance...

For example:

- Blast_UI standard use on home site
- Builds URL based track for hits →
- Can be aimed anywhere with the same database...

BLAST Results

Download: [Alignment](#), [Tab-Delimited](#), [GFF3](#), [XML](#)

Visualization: [JBrowse](#) (location will be set to the first hit)

[https://peanutbase.org/node/319881/?data=Aradu1.0&addTracks=\[{"label"%3A"blast"%2C"store"%3A"url"%2C"type"%3A"JBrowse%2FView%2FTrack%2FCanvasFeatures"%2C...](https://peanutbase.org/node/319881/?data=Aradu1.0&addTracks=[{)



PeanutBase

Genetic and genomic data to enable more rapid crop improvement in peanut.

[Contact us](#)

[Newsletter signup](#)

[Home](#) [Species](#) [Browse & Search](#) [Traits & Maps](#) [Germplasm](#) [Download](#) [Submit Data](#) [Community](#) [External](#) [Help](#)

Show URL for Bookmark

Available Tracks

✕ filter tracks

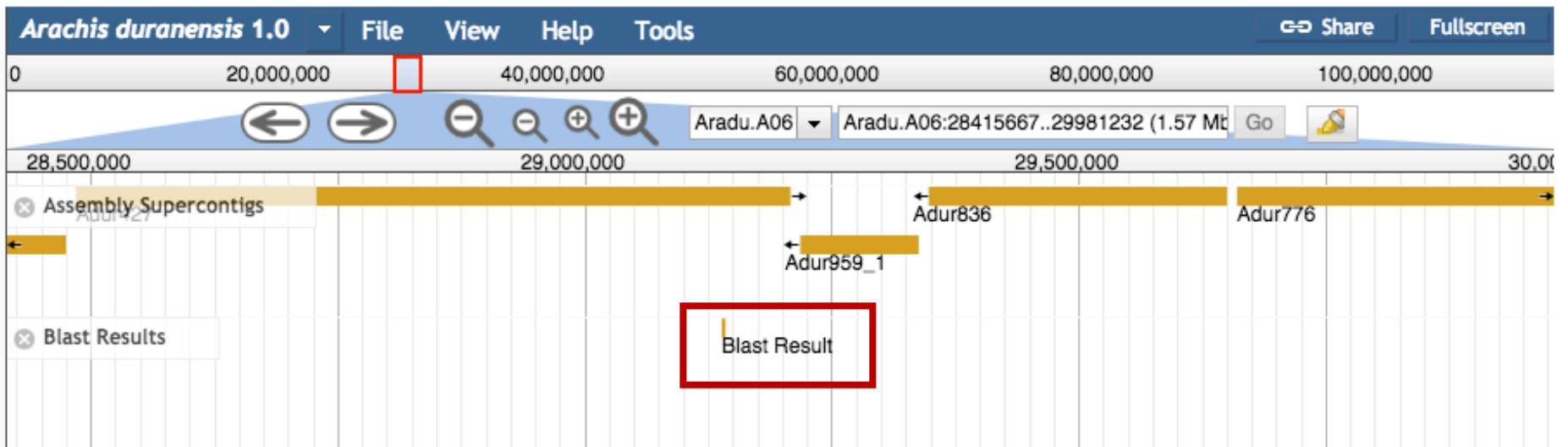
☒ Blast Results

▼ General 1

☒ Assembly Supercontigs

▼ Genes 5

- ☐ *Glycine max*2.0 gene models
- ☐ *Phaseolus vulgaris* gene models
- ☐ Gene models-Aradu.V14167.a1.G1
- ☐ Gene models-Aradu.V14167.a1.M1
- ☐ Gene models-Aradu.V14167.a1.NCBI



Why would you do this?

BLAST Results

Download: [Alignment](#), [Tab-Delimited](#), [GFF3](#), [XML](#)

Visualization: [JBrowse](#) (location will be set to the first hit)

Visualization: [JBrowse](#) (location will be set to the first hit)

→ To your own browser with unpublished data

→ To main resource browser with more tracks

Contrived example, but:

- Reduces clutter on your own browser
- Requires less resources to run, without sacrificing data available

Implementation

- Set up is the same as Blast_UI
- Will be available on our GitHub
 - Needs to have configuration added to the GUI
 - Changes are to two files: theme/blast_report.trp.php, and api/blast_ui.api.inc
 - Both updates are marked, current set up requires manual edits
 - README (soon to be help page) walks through how to set it up

DISCLAIMER: This is the first thing I ever modified in Tripal – but it's easy to do, so I use it on all of our sites ^_^.

Tools: Pop Up JB

A GUI-based web tool to spin up new JBrowse instances, with **on-the-fly track addition/removal by community**, allowing for more flexible community visualization.

[HOME](#)[GENOME BROWSER](#)[BLAST](#)

[Home](#) » [Genome Browser](#) » Load a New JBrowse Reference

Load a New JBrowse Reference

[View](#)[Edit](#)[Grant](#)

If you already have a reference loaded, please proceed to [here](#)

Reference Information

Reference Name (no spaces):

Select file to upload:

[Choose File](#)

No file chosen

[Submit](#)

Security through Node Access

Delete a Track Dark Eyed Junco Genome Resources

[VIEW](#)[EDIT](#)[GRANT](#)[Home](#) » [Genome Browser](#) » [Delete a Track](#)

You can set grants for individual users. Enter a name or a partial name in the box and click Search or press return. You must check the 'Keep?' checkbox if you want to keep the user for granting. Note that user grants are in addition to those coming from roles.

ROLE	VIEW	EDIT	DELETE
administrator	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
anonymous user	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
authenticated user	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

Enter names to search for users:

[HOME](#)[GENOME BROWSER](#)[BLAST](#)

[Home](#) » [Genome Browser](#) » Load a New JBrowse Reference

Load a New JBrowse Reference

[View](#)[Edit](#)[Grant](#)

If you already have a reference loaded, please proceed to [here](#)

Reference Information

Reference Name (no spaces):

Select file to upload:

No file chosen

Checks if file is *.fa or *.fasta, tells you if/why it fails.

Generally requires increased upload limit in php.ini

Browser Information

If you don't already have a reference loaded, please start with [here](#). Note: Available to Admins only.

Target Reference Name (no spaces - i.e. junco_26jun):

New Track Information

Track File Type:

✓ BAM
BED
GFF
GBK
VCF

(no spaces):

Select data to upload:

Choose File No file chosen

Submit

- Checks to make sure file extension is appropriate for the selected option.
- All commands are through samtools and JBrowse scripts, which check file format.

Delete a Track

[View](#)[Edit](#)[Grant](#)

Browser Information

Reference Name Used (no spaces - listed in browser URL after data =):

Target Track Information

Target Track Label (as listed in browser):

THIS WILL PERMENANTLY DELETE THE TRACK AND DATA. IT IS NOT REVERSABLE!

Implementation

- Install module as usual
- Have to boost php upload limit
- Have to put an “uploads” folder in JBrowse and open it to apache. I recommend putting a timed purge on uploads/tracks.
- If you are running a frozen version (without track modulation), which is RECOMMENDED, must be non-writable by apache.
- Extensive help page with commands to install dependencies (samtools, bioperl)
- Configure page to define path to JBrowse installation

Track flexibility is potentially very useful for popgen

Daphnia project with 96 samples from 96 populations...

- If you want to visualize data for different subsets of that data, this module allows for easy control of authorized users to add and remove tracks to visualize different subsets.
- More attractive than the alternatives of having a highly available admin (not an option in our case) or huge browsers (also not really an option).

Tools: Ready to Run Jetstream VM

We also build a virtual machine image built on the XSEDE cloud (Jetstream) with Tripal, JBrowse, and these tools installed - allowing for **free genome browser hosting with minimal command line** use and set up.



 [Tripal and Jbrowse on Ubuntu](#)

● Active

Initializing

149.165.169.113

M1.Medium

Jetstream - Indiana University



Popup Browser

Powered by NCGAS @ Indiana University

HOME

GENOME BROWSER

TOOLS

CONTACT

Welcome to the Pop Up Browser

Scope of Purpose

- visualize personal data
- get started on collaboration quickly
- start on hosted site

NOTES ON SIZE OF VM

- small is best for hosting (slow use of SUs)
- medium is required for loading large VMs
- you can start as medium, image, and relaunch as small

Features

PopUp JBrowse
BLAST w JBrowse links
Tripal Job Daemon

User login

Username *

Password *

✦ [Create new account](#)

✦ [Request new password](#)

Log in

Set Up and Use

JBrowse:

- see [Help for PopUp JB](#)
- once you have built it, add link to GENOME BROWSERS tab (edit the page, fill in the URL and title for the button to work!)

BLAST:

- make a blast reference
- upload it (via [globus](#) or [jetstream shell/web gui](#))
- add reference (add content -> Blast Database)

If you are going public:

- change your password!

```
cd /var/www/html/
```

```
sudo drush upwd --password="MyNewPassword" admin
```

This is an image – it has a built in password – which needs to be changed if you are going have the site persist.

I do have an account built in for me on the VM, so I can assist with anything anyone needs, as many of our clients are not command line/apache savvy.

This has really helpful in getting people started or running workshop/demos on tripal options without having to walk everyone through installing php/apache/etc.

Also, has made my life much easier, as I can start at a “save point” in the set up process when setting something up for our clients.

Jetstream Access

NCGAS holds three “community” allocations:

- Genomics*
- Field stations*
- Workshops

We help get everyone comfortable with JS and convinced whether or not it will be appropriate for them. Then they can get their own allocations, a process with which we can also help.

Joys of Jetstream

Really good idea to have development and production set ups

- Jetstream SUs get burned faster on larger VMs. Larger VMs are required for more memory – which is needed for **building references/tracks**, but not necessarily displaying them.
- Solution - have a development VM you boot only when needed, use globus to transfer track files between development and production
 - XSEDE users automatically qualify for globus plus (we have tutorials on how to get that)
 - We have walkthroughs on adding globus to a Jetstream instance.

Summary

Tool:

Blast_UI tweak

Popup_JB

Jetstream VM

Purpose:

shows blast results in internal/external JBrowse sites

on-the-fly track addition/removal by community

free genome browser hosting with minimal command line

How to find our tools

- Github (soon)
- Jetstream (by request)
- Email (help@ncgas.org)
- Website will have demos/tutorial to go with JS image soon!